

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/914,001

DATE: 09/10/2001
TIME: 11:28:54

Input Set : A:\Methy11.app
Output Set: N:\CRF3\09102001\I914001.raw

ENTERED

3 <110> APPLICANT: Wisconsin Alumni Research Foundation et al.
4 Pioneer Hi-Bred, International Inc.
5 Regents of The University of Minnesota
6 Kaeppler, Shawn M.
7 Springer, Nathan M.
8 Muszynski, Michael G.
9 Papa, Charles M.
11 <120> TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Encoding Class II
12 DNA Methyltransferases
14 <130> FILE REFERENCE: WIS4987P0051PCT
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/914,001
C--> 17 <141> CURRENT FILING DATE: 2001-08-20
19 <160> NUMBER OF SEQ ID NOS: 90
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2736
25 <212> TYPE: DNA
26 <213> ORGANISM: Zea mays
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31 tccgccaaagc gcagccgcaa ggcgcatct tccgggaaga agcccaagtc gcccccaag 180
32 caggccaagc cggggaggaa gaagaagggg gatgccgaga tgaaggagcc cgtggaggac 240
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37 gcaaagaaac cggatgagga ggaagagctc aaggccagat gtcactaccg gagcgctaag 540
38 gtggacaacg tcgtctactg cctcggggat gacgtctatg tcaaggctgg agaaaacgag 600
39 gcagattaca ttggccgcat tactgaattt tttagggga ctgaccagtg tcactatttt 660
40 acttgccgtt ggttcttccg agcagaggac acggttatca attctttggt gtccataagt 720
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57 gtggtggaca tactcaaatt tgcggtatggt tacctaggaa aatatgcttt gagctgcctt 1740
58 gttgctatga agtaccgaagc gcggcttgga atgatggtgg ctggttgcta tgggtctgcca 1800
59 cagttcagga tgcgtgtggt cctctgggggt gctctttctt ccatggtgct ccctaagtat 1860
60 cctctgcccc cctatgatgt tgtagtacgt ggaggagccc ctaatgcctt ttogcaatgt 1920
61 atggttgcat atgacgagac acaaaaacca tccctgaaaa aagccttgct tcttggcgat 1980
62 gcaatttcag atttaccaaa ggttcaaaat caccagccta acgatgtgat ggagtatggt 2040
63 ggttcccccag agaccgaatt ccagcgtctac attcgactca gtcgtaaaga catgttggat 2100
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65 cggcttaaca acgatgatta tgagcgggtt caacagattc ctgtcaagaa gggagccaac 2220
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67 atcgagcgtg tgaacttttc atctgggaaa ccactggttc ctgactatgc aatgtcattc 2340
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69 gttgtaacca gagcagagcc tcacaaccag gttataattc atccgactca agcaagggtc 2460
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73 cagctgcctc caagtttcac ctctgttggg ggacgcactg cggggcaggc gagggcctct 2700
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79 <212> TYPE: DNA
80 <213> ORGANISM: Zea mays
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85 gaggaggagg aggaggtcgc ggcggcgctc tccgccaagc gcagccgcaa ggcggcatct 180
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92 aaggccagat gtcactaccg gagcgctaag gtggacaacg tcgtctactg cctcggggat 600
93 gacgtctatg tcaaggctgg agaaaacgag gcagattaca ttggccgcat tactgaattt 660
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95 acggttatca attctttggt gtccataagt gtggatggcc acaagcatga ccctagacgt 780
96 gtttttcttt ctgaggaaaa gaacgacaat gtgcttgatt gcattatctc caaggtcaag 840
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107 cctgaggagg atacatggga accgattgat aacttgagtg actgcccgca gaaaattaga 1500
108 gaatttgtac aagaagggca caaaagaaa attctccac tgctgggtga tgttgatgtc 1560

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109 atttgtggag gccaccatg ccaaggtatc agtgggttta atcggtacag aaaccgtgat 1620
110 gagccactca aagatgagaa aaacaaacaa atggtgactt tcatggatat tgtggcgtag 1680
111 ttgaagccca agtatgttct catggaaaat gtggtggaca tactcaaatt tgcggatggg 1740
112 tacctaggaa aatatgcttt gagctgcctt gttgctatga agtaccaagc gcggcttgga 1800
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114 gctcttttct ccattggtct ccctaagtat cctctgcccc cctatgatgt ttagtagcgt 1920
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116 tccctgaaaa aagccttgct tcttgccgat gcaatttcag atttaccaaa ggttcaaaat 2040
117 caccagccta acgatgtgat ggagtatggg ggttccccca agaccgaatt ccagcgctac 2100
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123 cgctgtggg gggacgagac agttcctaca gttgtaacca gagcagagcc tcacaaccag 2460
124 gttataattc atccgactca agcaagggtc ctactatcc gggagaacgc aagggttacg 2520
125 ggcttccccg attactaccg attgtttggc ccgatcaagg agaagtacat tcaagtcggg 2580
126 aacgcagtgg ctgtccctgt tgcccgggca ctgggctact gtctggggca agcctacctg 2640
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128 ggacgcactg cggggcaggc gagggcctct cctgttgcca ccctgcagg ggaggtagtt 2760
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132 <210> SEQ ID NO: 3

133 <211> LENGTH: 912

134 <212> TYPE: PRT

135 <213> ORGANISM: Zea mays

137 <400> SEQUENCE: 3

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144 Glu Glu Glu Val Gly Ala Ala Ala Ser Ser Ala Lys Arg Ser Arg Lys
145           35           40           45
147 Ala Ala Ser Ser Gly Lys Lys Pro Lys Ser Pro Pro Lys Gln Ala Lys
148           50           55           60
150 Pro Gly Lys Lys Lys Gly Asp Ala Glu Met Lys Glu Pro Val Glu Asp
151  65           70           75           80
153 Asp Val Cys Ala Glu Glu Pro Asp Glu Glu Glu Leu Ala Met Gly Glu
154           85           90           95
156 Glu Glu Ala Glu Glu Gln Ala Met Gln Glu Glu Val Val Ala Val Ala
157           100          105          110
159 Ala Gly Ser Pro Gly Lys Lys Arg Val Gly Arg Arg Asn Ala Ala Ala
160           115          120          125
162 Ala Ala Gly Asp His Glu Pro Glu Phe Ile Gly Ser Pro Val Ala Ala
163           130          135          140
165 Asp Glu Ala Arg Ser Asn Trp Pro Lys Arg Tyr Gly Arg Ser Thr Ala
166 145           150          155          160
168 Ala Lys Lys Pro Asp Glu Glu Glu Glu Leu Lys Ala Arg Cys His Tyr
169           165          170          175
171 Arg Ser Ala Lys Val Asp Asn Val Val Tyr Cys Leu Gly Asp Asp Val

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| 172 | | | | 180 | | | | 185 | | | | 190 | | | | |
| 174 | Tyr | Val | Lys | Ala | Gly | Glu | Asn | Glu | Ala | Asp | Tyr | Ile | Gly | Arg | Ile | Thr |
| 175 | | | 195 | | | | | 200 | | | | | 205 | | | |
| 177 | Glu | Phe | Phe | Glu | Gly | Thr | Asp | Gln | Cys | His | Tyr | Phe | Thr | Cys | Arg | Trp |
| 178 | | 210 | | | | | 215 | | | | | 220 | | | | |
| 180 | Phe | Phe | Arg | Ala | Glu | Asp | Thr | Val | Ile | Asn | Ser | Leu | Val | Ser | Ile | Ser |
| 181 | 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| 183 | Val | Asp | Gly | His | Lys | His | Asp | Pro | Arg | Arg | Val | Phe | Leu | Ser | Glu | Glu |
| 184 | | | | 245 | | | | | | 250 | | | | | 255 | |
| 186 | Lys | Asn | Asp | Asn | Val | Leu | Asp | Cys | Ile | Ile | Ser | Lys | Val | Lys | Ile | Val |
| 187 | | | | 260 | | | | | 265 | | | | | 270 | | |
| 189 | His | Val | Asp | Pro | Asn | Met | Asp | Pro | Lys | Ala | Lys | Ala | Gln | Leu | Ile | Glu |
| 190 | | | 275 | | | | | 280 | | | | | | 285 | | |
| 192 | Ser | Cys | Asp | Leu | Tyr | Tyr | Asp | Met | Ser | Tyr | Ser | Val | Ala | Tyr | Ser | Thr |
| 193 | | 290 | | | | | 295 | | | | | 300 | | | | |
| 195 | Phe | Ala | Asn | Ile | Ser | Ser | Glu | Asn | Gly | Gln | Ser | Gly | Ser | Asp | Thr | Ala |
| 196 | 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| 198 | Ser | Gly | Ile | Ser | Ser | Asp | Asp | Val | Asp | Leu | Glu | Thr | Ser | Ser | Ser | Met |
| 199 | | | | 325 | | | | | | 330 | | | | | 335 | |
| 201 | Pro | Thr | Arg | Thr | Ala | Thr | Leu | Leu | Asp | Leu | Tyr | Ser | Gly | Cys | Gly | Gly |
| 202 | | | | 340 | | | | | 345 | | | | | 350 | | |
| 204 | Met | Ser | Thr | Gly | Leu | Cys | Leu | Gly | Ala | Ala | Leu | Ser | Gly | Leu | Lys | Leu |
| 205 | | | 355 | | | | | 360 | | | | | 365 | | | |
| 207 | Glu | Thr | Arg | Trp | Ala | Val | Asp | Phe | Asn | Ser | Phe | Ala | Cys | Gln | Ser | Leu |
| 208 | | 370 | | | | | 375 | | | | | 380 | | | | |
| 210 | Lys | Tyr | Asn | His | Pro | Gln | Thr | Glu | Val | Arg | Asn | Glu | Lys | Ala | Asp | Glu |
| 211 | 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| 213 | Phe | Leu | Ala | Leu | Leu | Lys | Glu | Trp | Ala | Val | Leu | Cys | Lys | Lys | Tyr | Val |
| 214 | | | | 405 | | | | | | 410 | | | | | 415 | |
| 216 | Gln | Asp | Val | Asp | Ser | Asn | Leu | Ala | Ser | Ser | Glu | Asp | Gln | Ala | Asp | Glu |
| 217 | | | | 420 | | | | | 425 | | | | | 430 | | |
| 219 | Asp | Ser | Pro | Leu | Asp | Lys | Asp | Glu | Phe | Val | Val | Glu | Lys | Leu | Val | Gly |
| 220 | | | 435 | | | | | 440 | | | | | 445 | | | |
| 222 | Ile | Cys | Tyr | Gly | Gly | Ser | Asp | Arg | Glu | Asn | Gly | Ile | Tyr | Phe | Lys | Val |
| 223 | | 450 | | | | 455 | | | | | 460 | | | | | |
| 225 | Gln | Trp | Glu | Gly | Tyr | Gly | Pro | Glu | Glu | Asp | Thr | Trp | Glu | Pro | Ile | Asp |
| 226 | 465 | | | | | 470 | | | | | 475 | | | | 480 | |
| 228 | Asn | Leu | Ser | Asp | Cys | Pro | Gln | Lys | Ile | Arg | Glu | Phe | Val | Gln | Glu | Gly |
| 229 | | | | 485 | | | | | | 490 | | | | | 495 | |
| 231 | His | Lys | Arg | Lys | Ile | Leu | Pro | Leu | Pro | Gly | Asp | Val | Asp | Val | Ile | Cys |
| 232 | | | | 500 | | | | | 505 | | | | | 510 | | |
| 234 | Gly | Gly | Pro | Pro | Cys | Gln | Gly | Ile | Ser | Gly | Phe | Asn | Arg | Tyr | Arg | Asn |
| 235 | | | 515 | | | | | 520 | | | | | 525 | | | |
| 237 | Arg | Asp | Glu | Pro | Leu | Lys | Asp | Glu | Lys | Asn | Lys | Gln | Met | Val | Thr | Phe |
| 238 | | 530 | | | | 535 | | | | | | 540 | | | | |
| 240 | Met | Asp | Ile | Val | Ala | Tyr | Leu | Lys | Pro | Lys | Tyr | Val | Leu | Met | Glu | Asn |
| 241 | 545 | | | | | 550 | | | | | 555 | | | | 560 | |
| 243 | Val | Val | Asp | Ile | Leu | Lys | Phe | Ala | Asp | Gly | Tyr | Leu | Gly | Lys | Tyr | Ala |
| 244 | | | | 565 | | | | | 570 | | | | | 575 | | |

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246 Leu Ser Cys Leu Val Ala Met Lys Tyr Gln Ala Arg Leu Gly Met Met
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252 Trp Gly Ala Leu Ser Ser Met Val Leu Pro Lys Tyr Pro Leu Pro Thr
253          610          615          620
255 Tyr Asp Val Val Val Arg Gly Gly Ala Pro Asn Ala Phe Ser Gln Cys
256 625          630          635          640
258 Met Val Ala Tyr Asp Glu Thr Gln Lys Pro Ser Leu Lys Lys Ala Leu
259          645          650          655
261 Leu Leu Gly Asp Ala Ile Ser Asp Leu Pro Lys Val Gln Asn His Gln
262          660          665          670
264 Pro Asn Asp Val Met Glu Tyr Gly Gly Ser Pro Lys Thr Glu Phe Gln
265          675          680          685
267 Arg Tyr Ile Arg Leu Ser Arg Lys Asp Met Leu Asp Trp Ser Phe Gly
268          690          695          700
270 Glu Gly Ala Gly Pro Asp Glu Gly Lys Leu Leu Asp His Gln Pro Leu
271 705          710          715          720
273 Arg Leu Asn Asn Asp Asp Tyr Glu Arg Val Gln Gln Ile Pro Val Lys
274          725          730          735
276 Lys Gly Ala Asn Phe Arg Asp Leu Lys Gly Val Arg Val Gly Ala Asn
277          740          745          750
279 Asn Ile Val Glu Trp Asp Pro Glu Ile Glu Arg Val Lys Leu Ser Ser
280          755          760          765
282 Gly Lys Pro Leu Val Pro Asp Tyr Ala Met Ser Phe Ile Lys Gly Lys
283          770          775          780
285 Ser Leu Lys Pro Phe Gly Arg Leu Trp Trp Asp Glu Thr Val Pro Thr
286 785          790          795          800
288 Val Val Thr Arg Ala Glu Pro His Asn Gln Val Ile Ile His Pro Thr
289          805          810          815
291 Gln Ala Arg Val Leu Thr Ile Arg Glu Asn Ala Arg Leu Gln Gly Phe
292          820          825          830
294 Pro Asp Tyr Tyr Arg Leu Phe Gly Pro Ile Lys Glu Lys Tyr Ile Gln
295          835          840          845
297 Val Gly Asn Ala Val Ala Val Pro Val Ala Arg Ala Leu Gly Tyr Cys
298          850          855          860
300 Leu Gly Gln Ala Tyr Leu Gly Glu Ser Glu Gly Ser Asp Pro Leu Tyr
301 865          870          875          880
303 Gln Leu Pro Pro Ser Phe Thr Ser Val Gly Gly Arg Thr Ala Gly Gln
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314 <211> LENGTH: 922
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316 <213> ORGANISM: Zea mays
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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date